

## SEQUENCE LISTING

<110> CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE, INC.

<120> NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10

<130> C2-105DP1PCT

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<150> JP1999-155797

<151> 1999-06-02

<150> JP1999-217797

<151> 1999-07-30

<160> 20

<170> PatentIn Ver. 2.0

<210> 1

<211> 2969

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (523).. (2478)

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accagcatgg tactaaatag accatgaaaa gacatgtgtg tgcagtatga aaattgagac 180

aggaaggcag agtgtcagct tgttccacct cagctgggaa tgtgcatcag gcaactcaag 240

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aaagctcgca gacaatcaga gtggaaacac tcccacatct tagtgtggat aaattaaagt 420

ccagattgtt ctctctgtcc tgacttgtgc tgtgggaggt ggagttgcct ttgatgaaa 480

tcctttgagc cagcagaaca tctgtggaac atcccctgat ac atg aag ctc tct 534

Met Lys Leu Ser

1

ccc cag cct tca tgt gtt aac ctg ggg atg atg tgg acc tgg gca ctg 582

Pro Gln Pro Ser Cys Val Asn Leu Gly Met Met Trp Thr Trp Ala Leu  
 5 10 15 20

tgg atg etc ccc tca etc tgc aaa ttc agc ctg gca gct ctg cca gct 630  
 Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu Pro Ala  
 25 30 35

aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat tta acc 678  
 Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg Lys Asn Leu Thr  
 40 45 50

tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac aca gtt 726  
 Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr Thr Val  
 55 60 65

aag aga act tac gct ttc gga gaa aaa cat gat aat tgt aca acc aat 774  
 Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn Cys Thr Thr Asn  
 70 75 80

agt tct aca agt gaa aat cgt gct tcg tgc tct ttt ttc ctt cca aga 822  
 Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe Phe Leu Pro Arg  
 85 90 95 100

ata acg atc cca gat aat tat acc att gag gtg gaa gct gaa aat gga 870  
 Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu Ala Glu Asn Gly  
 105 110 115

gat ggt gta att aaa tct cat atg aca tac tgg aga tta gag aac ata 918

Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg Leu Glu Asn Ile

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gcg aaa act gaa cca cct aag att ttc cgt gtg aaa cca gtt ttg ggc 966

Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys Pro Val Leu Gly

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atc aaa cga atg att caa att gaa tgg ata aag cct gag ttg gcg cct 1014

Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro Glu Leu Ala Pro

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gtt tca tct gat tta aaa tac aca ctt cga ttc agg aca gtc aac agt 1062

Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg Thr Val Asn Ser

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acc agc tgg atg gaa gtc aac ttc gct aag aac cgt aag gat aaa aac 1110

Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg Lys Asp Lys Asn

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caa acg tac aac ctc acg ggg ctg cag cct ttt aca gaa tat gtc ata 1158

Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr Glu Tyr Val Ile

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gct ctg cga tgt gcg gtc aag gag tca aag ttc tgg agt gac tgg agc 1206

Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp Ser Asp Trp Ser

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caa gaa aaa atg gga atg act gag gaa gaa gct cca tgt ggc ctg gaa 1254

Gln Glu Lys Met Gly Met Thr Glu Glu Glu Ala Pro Cys Gly Leu Glu

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ctg tgg aga gtc ctg aaa cca gct gag ggc gat gga aga agg cca gtg 1302

Leu Trp Arg Val Leu Lys Pro Ala Glu Ala Asp Gly Arg Arg Pro Val

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cgg ttg tta tgg aag aag gca aga gga gcc cca gtc cta gag aaa aca 1350

Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val Leu Glu Lys Thr

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ctt ggc tac aac ata tgg tac tat cca gaa agc aac act aac ctc aca 1398

Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn Thr Asn Leu Thr

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gaa aca atg aac act act aac cag cag ctt gaa ctg cat ctg gga ggc 1446

Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu His Leu Gly Gly

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gag agc ttt tgg gtg tet atg att tet tat aat tet ctt ggg aag tet 1494

Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser Leu Gly Lys Ser

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cca gtg gcc acc ctg agg att cca gct att caa gaa aaa tca ttt cag 1542

Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu Lys Ser Phe Gln

325 330 335 340

tgc att gag gtc atg cag gcc tgc gtt gct gag gac cag cta gtg gtg 1590

Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp Gln Leu Val Val

345 350 355

aag tgg caa agc tct gct cta gac gtg aac act tgg atg att gaa tgg 1638

Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp Met Ile Glu Trp

360 365 370

ttt ccg gat gtg gac tca gag ccc acc acc ctt tcc tgg gaa tct gtg 1686

Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser Trp Glu Ser Val

375 380 385

tct cag gcc acg aac tgg acg atc cag caa gat aaa tta aaa cct ttc 1734

Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys Leu Lys Pro Phe

390 395 400

tgg tgc tat aac atc tct gtg tat cca atg ttg cat gac aaa gtt ggc 1782

Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His Asp Lys Val Gly

405 410 415 420

gag cca tat tcc atc cag gct tat gcc aaa gaa ggc gtt cca tca gaa 1830

Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly Val Pro Ser Glu

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ggt cct gag acc aag gtg gag aac att ggc gtg aag acg gtc acg atc 1878

Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys Thr Val Thr Ile

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aca tgg aaa gag att ccc aag agt gag aga aag ggt atc atc tgc aac 1926

Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys Gly Ile Ile Cys Asn

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tac acc atc ttt tac caa gct gaa ggt gga aaa gga ttc tcc aag aca 1974

Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly Phe Ser Lys Thr

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gtc aat tcc agc atc ttg cag tac ggc ctg gag tcc ctg aaa cga aag 2022

Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser Leu Lys Arg Lys

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acc tct tac att gtt cag gtc atg gcc aac acc agt gct ggg gga acc 2070

Thr Ser Tyr Ile Val Gln Val Met Ala Asn Thr Ser Ala Gly Gly Thr

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510

515

aac ggg acc agc ata aat ttc aag aca ttg tca ttc agt gtc ttt gag 2118

Asn Gly Thr Ser Ile Asn Phe Lys Thr Leu Ser Phe Ser Val Phe Glu

520

525

530

Ile Ile Leu Ile Thr Ser Leu Ile Gly Gly Gly Leu Leu Ile Leu Ile

540

545

Ile Leu Thr Val Ala Tyr Gly Leu Lys Lys Pro Asn Lys Leu Thr His

550

555

560

Leu Cys Trp Pro Thr Val Pro Asn Pro Ala Glu Ser Ser Ile Ala Thr

565

570

575

580

Trp His Gly Asp Asp Phe Lys Asp Lys Leu Asn Leu Lys Glu Ser Asp

585

590

595

Asp Ser Val Asn Thr Glu Asp Arg Ile Leu Lys Pro Cys Ser Thr Pro

600

605

610

Ser Asp Lys Leu Val Ile Asp Lys Leu Val Val Asn Phe Gly Asn Val

615

620

625

ctg caa gaa att ttc aca gat gaa gcc aga acg ggt cag gaa aaa caa 2454



Leu Gln Glu Ile Phe Thr Asp Glu Ala Arg Thr Gly Gln Glu Lys Gln

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640

ttt agg agg gga aaa gaa tgg gac tagaattctg tcttcctgcc caacttcaat 2508

Phe Arg Arg Gly Lys Glu Trp Asp

645

650

ataagtgtgg actaaaatgc gagaaagggtg tcctgtgggtc tatgcaaatt agaaaggaca 2568

tgcagagttt tccaactagg aagactgaat ctgtggcccc aagagaacca tctccgaaga 2628

ctgggtatgt ggtcttttcc acacatggac cacctacgga tgcaatctgt aatgcatgtg 2688

catgagaagt ctgttattaa gtagagtgtg aaaacatggt tatggtaata ggaacagett 2748

ttaaaatgct tttgtatttg ggcctttcac acaaaaaaagc cataatacca ttttcatgta 2808

atgctatact tctatactat tttcatgtaa tactatactt ctatactatt ttcatgtaat 2868

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2969

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<211> 652

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala

20 25 30

Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg

35 40 45

Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr

50 55 60

Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn

65 70 75 80

Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe

85 90 95

Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu

100 105 110

Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg

115 120 125  
Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys  
130 135 140  
Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro  
145 150 155 160  
Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg  
165 170 175  
Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg  
180 185 190  
Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr  
195 200 205  
Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp  
210 215 220  
Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Ala Pro  
225 230 235 240  
Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu Ala Asp Gly  
245 250 255

Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val

260

265

270

Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn

275

280

285

Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu

290

295

300

His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser

305

310

315

320

Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu

325

330

335

Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp

340

345

350

Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp

355

360

365

Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser

370

375

380

Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys

385

390

395

400

Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His

405

410

415

Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly

420

425

430

Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys

435

440

445

Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys Gly

450

455

460

Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly

465

470

475

480

Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser

485

490

495

Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala Asn Thr Ser

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505

510

Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr Leu Ser Phe

515

520

525

Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly Gly Gly Leu

530

535

540

Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys Lys Pro Asn

545

550

555

560

Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro Ala Glu Ser

565

570

575

Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys Leu Asn Leu

580

585

590

Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile Leu Lys Pro

595

600

605

Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu Val Val Asn

610

615

620

Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala Arg Thr Gly

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Gln Glu Lys Gln Phe Arg Arg Gly Lys Glu Trp Asp

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&lt;210&gt; 3

&lt;211&gt; 2440

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (523).. (1278)

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accagcatgg tactaaatag accatgaaaa gacatgtgtg tgcagtatga aaattgagac 180

aggaaggcag agtgtcagct tgttccacct cagctgggaa tgtgcatcag gcaactcaag 240

ttttcacca cggcatgtgt ctgtgaatgt ccgcaaaaca ttittaacaat aatgcaatcc 300

atttcccagc ataagtgggt aagtgccact ttgacttggg ctgggcttaa aagcacaaga 360

aaagctcgca gacaatcaga gtggaacac tcccacatct tagtgtggat aaattaaagt 420

ccagattgtt cttcctgtcc tgacttgtgc tgtgggaggt ggagttgcct ttgatgcaaa 480

tcctttgagc cagcagaaca tctgtggaac atcccctgat ac atg aag ctc tct 534

Met Lys Leu Ser

ccc cag cct tca tgt gtt aac ctg ggg atg atg tgg acc tgg gca ctg 582

Pro Gln Pro Ser Cys Val Asn Leu Gly Met Met Trp Thr Trp Ala Leu

5 10 15 20

tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg cca gct 630

Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu Pro Ala

25 30 35

aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat tta acc 678

Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg Lys Asn Leu Thr

40 45 50

tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac aca gtt 726

Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr Thr Val

55 60 65

aag aga act tac gct ttc gga gaa aaa cat gat aat tgt aca acc aat 774

Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn Cys Thr Thr Asn

70 75 80

agt tct aca agt gaa aat cgt gct tgc tgc tct ttt ttc ctt cca aga 822

Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe Phe Leu Pro Arg

85 90 95 100



ata acg atc cca gat aat tat acc att gag gtg gaa gct gaa aat gga 870

Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu Ala Glu Asn Gly

105

110

115

gat ggt gta att aaa tct cat atg aca tac tgg aga tta gag aac ata 918

Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg Leu Glu Asn Ile

120

125

130

gcg aaa act gaa cca cct aag att ttc cgt gtg aaa cca gtt ttg ggc 966

Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys Pro Val Leu Gly

135

140

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atc aaa cga atg att caa att gaa tgg ata aag cct gag ttg gcg cct 1014

Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro Glu Leu Ala Pro

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gtt tca tct gat tta aaa tac aca ctt cga ttc agg aca gtc aac agt 1062

Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg Thr Val Asn Ser

165

170

175

180

acc agc tgg atg gaa gtc aac ttc gct aag aac cgt aag gat aaa aac 1110

Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg Lys Asp Lys Asn

185

190

195

caa acg tac aac ctc acg ggg ctg cag cct ttt aca gaa tat gtc ata 1158

Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr Glu Tyr Val Ile

200

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gct ctg cga tgt gcg gtc aag gag tca aag ttc tgg agt gac tgg agc 1206

Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp Ser Asp Trp Ser

215

220

225

caa gaa aaa atg gga atg act gag gaa gaa ggc aag cta ctc cct gcg 1254

Gln Glu Lys Met Gly Met Thr Glu Glu Glu Gly Lys Leu Leu Pro Ala

230

235

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att ccc gtc ctg tct act ctg gtg tagggctgct ttgggctaga cttggtggg 1308

Ile Pro Val Leu Ser Thr Leu Val

245

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cgagagtgag cctgcacaac ttgtgtcccc aaaggcaaag gatcacattt taatactcat 1428

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<210> 4

<211> 252

<212> PRT

<213> Homo sapiens

<400> 4

Met Lys Leu Ser Pro Gln Pro Ser Cys Val Asn Leu Gly Met Met Trp

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Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala

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Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg

35 40 45

Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr

50 55 60

Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn

65 70 75 80

Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe

85 90 95

Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu

100

105

110

Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg

115

120

125

Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys

130

135

140

Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro

145

150

155

160

Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg

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175

Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg

180

185

190

Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr

195

200

205

Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp

210

215

220

Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Gly Lys

225

230

235

240

Leu Leu Pro Ala Ile Pro Val Leu Ser Thr Leu Val

245

250

&lt;210&gt; 5

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:Artificially  
Synthesized Oligonucleotide Primer Sequence

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atggaagtca acttcgctaa gaaccgtaag

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&lt;210&gt; 6

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:Artificially  
Synthesized Oligonucleotide Primer Sequence

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ccaaacgtac aacctcacgg ggctgcaacc

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<210> 7

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
Synthesized Oligonucleotide Primer Sequence

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gtcatagctc tgcgatgtgc ggtcaaggag

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<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
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<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
Syntthesized Oligonucleotide Primer Sequence

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<210> 10

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Artificially  
Syntthesized Oligonucleotide Primer Sequence



<400> 10

ggttgcagcc ccgtgaggtt gtacgtttgg

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<210> 11

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially  
Syntthesized Oligonucleotide Primer Sequence

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<210> 12

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially  
Syntthesized Oligonucleotide Primer Sequence

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<210> 13

<211> 27

<212> DNA

<213> Artificial Sequence

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Syntthesized Oligonucleotide Primer Sequence

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gcattcagga cagtcaacag taccagc

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<210> 14

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially  
Syntthesized Oligonucleotide Primer Sequence

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agctggaatc ctcagggtgg ccactgg

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<210> 15

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially  
Syntthesized Oligonucleotide Primer Sequence

<400> 15

gcccatacc agagtagaca ggacggg

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<210> 16

<211> 2119

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (11).. (1996)

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ccctgatac atg aag ctc tct ccc cag cct tca tgt gtt aac ctg ggg 49

Met Lys Leu Ser Pro Gln Pro Ser Cys Val Asn Leu Gly

1

5

10

atg atg tgg acc tgg gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc 97

Met Met Trp Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe

15

20

25

agc ctg gca gct ctg cca gct aag cct gag aac att tcc tgt gtc tac 145

Ser Leu Ala Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr

30

35

40

45

tac tat agg aaa aat tta acc tgc act tgg agt cca gga aag gaa acc 193

Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr

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agt tat acc cag tac aca gtt aag aga act tac gct ttt gga gaa aaa 241

Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys

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70

75

cat gat aat tgt aca acc aat agt tct aca agt gaa aat cgt gct tcg 289

His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser

80

85

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tgc tct ttt ttc ctt cca aga ata acg atc cca gat aat tat acc att 337

Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile

95

100

105

gag gtg gaa gct gaa aat gga gat ggt gta att aaa tct cat atg aca 385

Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr

110

115

120

125

tac tgg aga tta gag aac ata gcg aaa act gaa cca cct aag att ttc 433

Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe

130

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cgt gtg aaa cca gtt ttg ggc atc aaa cga atg att caa att gaa tgg 481

Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp

145

150

155

ata aag cct gag ttg gcg cct gtt tca tct gat tta aaa tac aca ctt 529

Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu

160

165

170

cga ttc agg aca gtc aac agt acc agc tgg atg gaa gtc aac ttc gct 577

Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala

175

180

185

aag aac cgt aag gat aaa aac caa acg tac aac ctc acg ggg ctg cag 625

Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln

190

195

200

205

cct ttt aca gaa tat gtc ata gct ctg cga tgt gcg gtc aag gag tca 673

Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser

210

215

220

aag ttc tgg agt gac tgg agc caa gaa aaa atg gga atg act gag gaa 721

Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu

225

230

235

gaa gct cca tgt ggc ctg gaa ctg tgg aga gtc ctg aaa cca gct gag 769

Glu Ala Pro Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu

240

245

250

gcg gat gga aga agg cca gtg cgg ttg tta tgg aag aag gca aga gga 817

Ala Asp Gly Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly

255

260

265

gcc cca gtc cta gag aaa aca ctt ggc tac aac ata tgg tac tat cca 865

Ala Pro Val Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro

270

275

280

285

gaa agc aac act aac ctc aca gaa aca atg aac act act aac cag cag 913

Glu Ser Asn Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln

290

295

300

ctt gaa ctg cat ctg gga ggc gag agc ttt tgg gtg tct atg att tct 961

Leu Glu Leu His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser

305

310

315

tat aat tct ctt ggg aag tct cca gtg gcc acc ctg agg att cca gct 1009

Tyr Asn Ser Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala

320

325

330

att caa gaa aaa tca ttt cag tgc att gag gtc atg cag gcc tgc gtt 1057

Ile Gln Glu Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val

335

340

345

gct gag gac cag cta gtg gtg aag tgg caa agc tct gct cta gac gtg 1105

Ala Glu Asp Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val

350

355

360

365

aac act tgg atg att gaa tgg ttt ccg gat gtg gac tca gag ccc acc 1153

Asn Thr Trp Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr

370

375

380

acc ctt tcc tgg gaa tct gtg tct cag gcc acg aac tgg acg atc cag 1201

Thr Leu Ser Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln

385

390

395

caa gat aaa tta aaa cct ttc tgg tgc tat aac atc tct gtg tat cca 1249

Gln Asp Lys Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro

400

405

410

atg ttg cat gac aaa gtt ggc gag cca tat tcc atc cag gct tat gcc 1297

Met Leu His Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala

415

420

425

aaa gaa ggc gtt cca tca gaa ggt cct gag acc aag gtg gag aac att 1345

Lys Glu Gly Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile

430

435

440

445

ggc gtg aag acg gtc acg atc aca tgg aaa gag att ccc aag agt gag 1393

Gly Val Lys Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu

450

455

460

aga aag ggt atc atc tgc aac tac acc atc ttt tac caa gct gaa ggt 1441

Arg Lys Gly Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly

465

470

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gga aaa gga ttc tcc aag aca gtc aat tcc agc atc ttg cag tac ggc 1489

Gly Lys Gly Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly

480

485

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ctg gag tcc ctg aaa cga aag acc tct tac att gtt cag gtc atg gcc 1537

Leu Glu Ser Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala

495

500

505

agc acc agt gct ggg gga acc aac ggg acc agc ata aat ttc aag aca 1585



Ser Thr Ser Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr

510 515 520 525

ttg tca ttc agt gtc ttt gag att atc ctc ata act tct ctg att ggt 1633

Leu Ser Phe Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly

530 535 540

gga ggc ctt ctt att ctc att atc ctg aca gtg gca tat ggt ctc aaa 1681

Gly Gly Leu Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys

545 550 555

aaa ccc aac aaa ttg act cat ctg tgt tgg ccc acc gtt ccc aac cct 1729

Lys Pro Asn Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro

560 565 570

gct gaa agt agt ata gcc aca tgg cat gga gat gat ttc aag gat aag 1777

Ala Glu Ser Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys

575 580 585

cta aac ctg aag gag tct gat gac tct gtg aac aca gaa gac agg atc 1825

Leu Asn Leu Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile

590 595 600 605

tta aaa cca tgt tcc acc ccc agt gac aag ttg gtg att gac aag ttg 1873

Leu Lys Pro Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu

610 615 620

gtg gtg aac ttt ggg aat gtt ctg caa gaa att ttc aca gat gaa gcc 1921

Val Val Asn Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala

625

630

635

aga acg ggt cag gaa aac aat tta gga ggg gaa aag aat ggg act aga 1969

Arg Thr Gly Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly Thr Arg

640

645

650

att ctg tct tcc tgc cca act tca ata taagtgtgga ctaaaatgcg 2016

Ile Leu Ser Ser Cys Pro Thr Ser Ile

655

660

agaaagggtgt cctgtggtct atgcaaatta gaaaggacat gcagagtttt ccaactagga 2076

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<212> PRT

<213> Homo sapiens

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Met Lys Leu Ser Pro Gln Pro Ser Cys Val Asn Leu Gly Met Met Trp

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Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala

20

25

30

Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg

35

40

45

Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr

50

55

60

Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn

65

70

75

80

Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe

85

90

95

Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu

100

105

110

Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg

115

120

125

Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys

130

135

140

Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro

145 150 155 160

Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg

165 170 175

Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg

180 185 190

Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr

195 200 205

Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp

210 215 220

Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Ala Pro

225 230 235 240

Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu Ala Asp Gly

245 250 255

Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val

260 265 270

Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn

275 280 285

Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu

290

295

300

His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser

305

310

315

320

Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu

325

330

335

Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp

340

345

350

Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp

355

360

365

Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser

370

375

380

Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys

385

390

395

400

Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His

405

410

415

Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly

420

425

430

Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys

435

440

445

Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys Gly

450

455

460

Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly

465

470

475

480

Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser

485

490

495

Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala Ser Thr Ser

500

505

510

Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr Leu Ser Phe

515

520

525

Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly Gly Gly Leu

530

535

540

Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys Lys Pro Asn

545

550

555

560

Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro Ala Glu Ser

565

570

575

Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys Leu Asn Leu

580

585

590

Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile Leu Lys Pro

595

600

605

Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu Val Val Asn

610

615

620

Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala Arg Thr Gly

625

630

635

640

Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly Thr Arg Ile Leu Ser

645

650

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Ser Cys Pro Thr Ser Ile

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&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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<223> Description of Artificial Sequence:Artificially  
Synthesized Oligonucleotide Primer Sequence

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<210> 19

<211> 30

<212> DNA

<213> Artificial Sequence

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Synthesized Oligonucleotide Primer Sequence

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<213> Artificial Sequence



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Synthesized Oligonucleotide Primer Sequence

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